

A

**MUSCLE-N**  
m MGGQITRNTIHD-----SIGGSFPVPS-----HRCHHKQKHCPTTSLG----

**BRAIN-N**  
m MGNFSSVSSSLQRGNSRASRG--EPQNLKE-----SIGGSFPVPS-----HRCHHKQKHCPTTSLG---- 55  
r MGNFSSVSSSLQRGNSRASRG--EPQNLKD-----SIGGSFPVPS-----HRCHHKQKHCPTTSLG---- 55  
h MGNFSSVSSSLQRGNSRASRG--EPQNLKD-----SIGGSFPVPS-----HRCHHKQKHCPTTSLG---- 55  
d MGLSDIPANYMQGSHHTLTPQQQSHNQHLQHLQMQQLHNAMPTPAQAAQVLAMESNELLMSTKDKLSSKKKKLLKKIKKRFGL 90

**NLS1**  
m -----GGLPATPLLFPHTRKSCQLMDLSHKAVKQASFCNAITFSNRPLYIEQVRLKITKQCCWSGALRLGFTSKDPSRIHPD 136  
r -----GGLPATPLLFPHTRKSCQLMDLSHKAVKQASFCNAITFSNRPLYIEQVRLKITKQCCWSGALRLGFTSKDPSRIHPD 136  
h -----GGLPATPLLFPHTRKSCQLMDLSHKAVKQASFCNAITFSNRPLYIEQVRLKITKQCCWSGALRLGFTSKDPSRIHPD 136  
d VRRSPSSCPFNNLPELOPH-SVHCNDRISRDTGLARFESFCRAITFSARPRIINERICVSFAEISNNNGGIRFGFTSNDF-VTLEG 178

**NLS2**  
m -----GGLPATPLLFPHTRKSCQLMDLSHKAVKQASFCNAITFSNRPLYIEQVRLKITKQCCWSGALRLGFTSKDPSRIHPD 136  
r -----GGLPATPLLFPHTRKSCQLMDLSHKAVKQASFCNAITFSNRPLYIEQVRLKITKQCCWSGALRLGFTSKDPSRIHPD 136  
h -----GGLPATPLLFPHTRKSCQLMDLSHKAVKQASFCNAITFSNRPLYIEQVRLKITKQCCWSGALRLGFTSKDPSRIHPD 136  
d VRRSPSSCPFNNLPELOPH-SVHCNDRISRDTGLARFESFCRAITFSARPRIINERICVSFAEISNNNGGIRFGFTSNDF-VTLEG 178

**NHR1**  
m SLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218  
r SLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTADPLWALVDVYGLTRGVQLLDS----- 218  
h SLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTADPLWALVDVYGLTRGVQLLDS----- 218  
d TLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTADPLWALVDVYGLTRGVQLLDSRIYMYQQQ 268

**LRS1 \***  
m SLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTVDFLWALVDVYGLTRGVQLLDS----- 218  
r SLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTADPLWALVDVYGLTRGVQLLDS----- 218  
h SLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTADPLWALVDVYGLTRGVQLLDS----- 218  
d TLPKYACPDVLSQSCEWAKALPEEFANECHIAFWVDKGRVRYRINESAAMLFFSGVRTADPLWALVDVYGLTRGVQLLDSRIYMYQQQ 268

**O**  
m ELVLDDCLRSFTALRRSLRCEADE-----ARLSVSICDLNVSGADGDDGAPPAG--CPIPONSLNSQHSRALE-A 288  
r ELVLDDCLRSFTALRRSLRCEADE-----ARLSVSICDLNVSGADGDDGAPPAG--CPIPONSLNSQHSRALE-A 288  
h ELVLDDCLRSFTALRRSLRCEADE-----ARLSVSICDLNVSGADGDDGAPPAG--CPIPONSLNSQHSRALE-A 288  
d PAALMATVDAQQQMPQDAANASSALNSHHPHQSSRRSLPGHTAIEHDLERHVMESLQSLHISGNGGSVASVEQAIAHDLANGEPPL 358

**PKB**  
m ELVLDDCLRSFTALRRSLRCEADE-----ARLSVSICDLNVSGADGDDGAPPAG--CPIPONSLNSQHSRALE-A 288  
r ELVLDDCLRSFTALRRSLRCEADE-----ARLSVSICDLNVSGADGDDGAPPAG--CPIPONSLNSQHSRALE-A 288  
h ELVLDDCLRSFTALRRSLRCEADE-----ARLSVSICDLNVSGADGDDGAPPAG--CPIPONSLNSQHSRALE-A 288  
d PAALMATVDAQQQMPQDAANASSALNSHHPHQSSRRSLPGHTAIEHDLERHVMESLQSLHISGNGGSVASVEQAIAHDLANGEPPL 358

**NHR2**  
m QLDG-----DLRFHALRAAHVRILDEQTVARLEHGRDERALVETSRPVVSAITIFIVTRSGGGRAGALSFGVTTCDPGTLPFADLFFS 373  
r QLDG-----DLRFHALRAAHVRILDEQTVARLEHGRDERALVETSRPVVSAITIFIVTRSGGGRAGALSFGVTTCDPGTLPFADLFFS 373  
h QLDG-----DLRFHALRAAHVRILDEQTVARLEHGRDERALVETSRPVVSAITIFIVTRSGGGRAGALSFGVTTCDPGTLPFADLFFS 373  
d RYNANGRLIPVPEHNT-KERNVLSQDRFVASRTESDFCQGYVETAREIRIGKLIVCLKTEQMYVGALALGLTSNEAMTQENDLEND 447

**LRS2 \***  
m PEALVDRKEFFAVCR-VPGPLHSGLDILGLVNNADGELHLSHNGAAGMOLCVASQPLMMLFSLHCAITQVRILGSTIMTERGGP----- 457  
r PEALVDRKEFFAVCR-VPGPLHSGLDILGLVNNADGELHLSHNGAAGMOLCVASQPLMMLFSLHCAITQVRILGSTIMTERGGP----- 457  
h PEALVDRKEFFAVCR-VPGPLHSGLDILGLVNNADGELHLSHNGAAGMOLCVASQPLMMLFSLHCAITQVRILGSTIMTERGGP----- 457  
d SDFELDRPEYVYVWSKDIAAPQRGEIAFFVAPNGEVSISKNGPQVVMHVDQSLQWAFLDVYGSTQSLMFRQQLPNMVAYESQPQV 537

**SP1**  
m -----SLPCSFASTFSPSALGIRLSD-----PLSTCGSGPLGGSAGG-----TAPNSPVSLPESVTPGLQWSD 519  
r -----SLPCSFASTFSPSALGIRLSD-----PLSTCGSGPLGGSAGG-----TAPNSPVSLPESVTPGLQWSD 519  
h -----SLPCSFASTFSPSALGIRLSD-----PLSTCGSGPLGGSAGG-----TAPNSPVSLPESVTPGLQWSD 519  
d NVNASSSSACNAASTSRMLPMTESMSLNAGATAKLLHHPSSLSVACSTSTLASAGGVNGSRMISMESNGDILQIQNGGGSTVLVNLPP 627

**O**  
m -----ECTICYEHAVDTVITTCG 537  
r -----ECTICYEHAVDTVITTCG 537  
h -----ECTICYEHAVDTVITTCG 537  
d ASSSHDINGQLAARPTATVTSVGLAGACSSGTLISTSSQYIEQPIANSTNNAANKWKDSLSDQSTDSSECTICYENPISVLMCG 717

**RZD**  
m HMCDCYSGLRLKKALH-ACCPICRRPKDIKTYRSS 574  
r HMCDCYSGLRLKKALH-ACCPICRRPKDIKTYRSS 574  
h HMCDCYSGLRLKKALH-ACCPICRRPKDIKTYRSS 574  
d HMCDCYDAIEQWRGVGGGQCPICRAVIRDVITYTT- 754

B

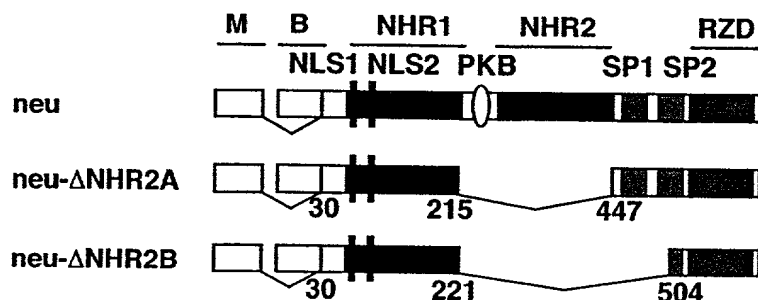
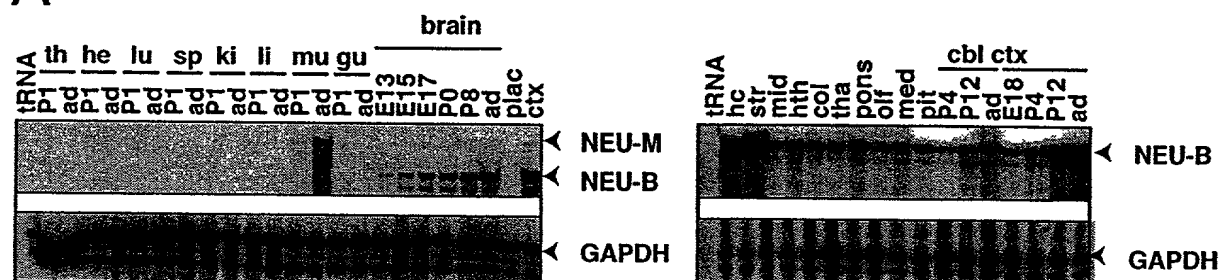


FIGURE 1

A



B

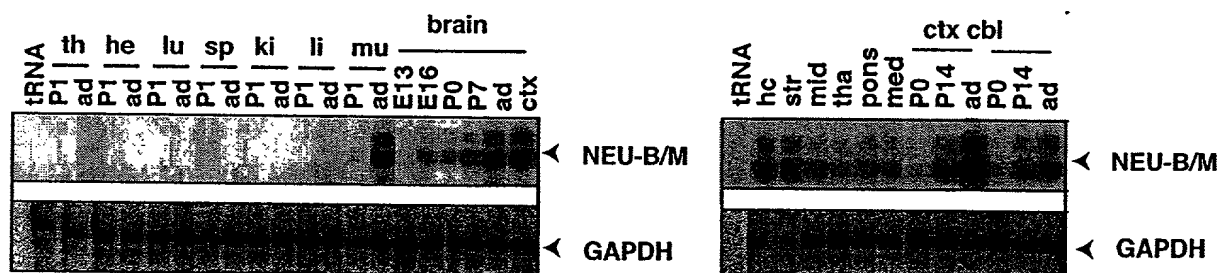


FIGURE 2

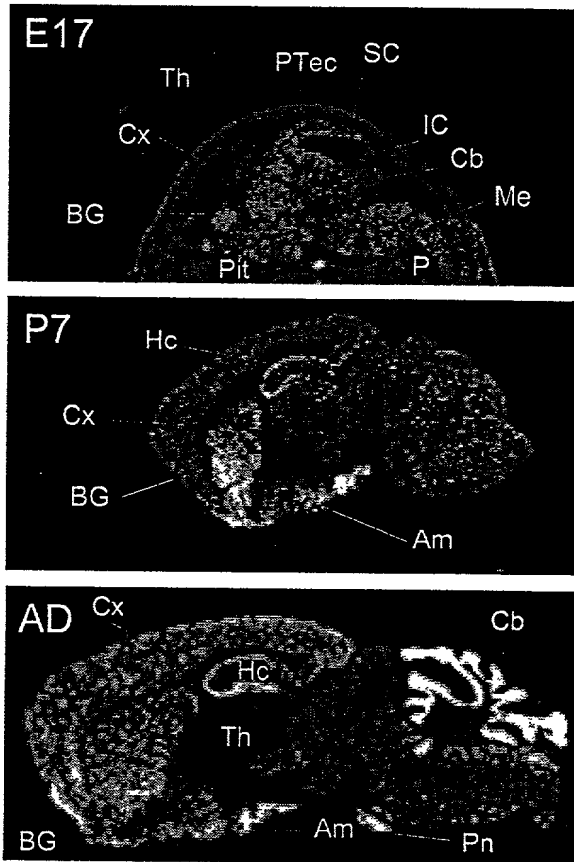


FIGURE 3

09803337-05201

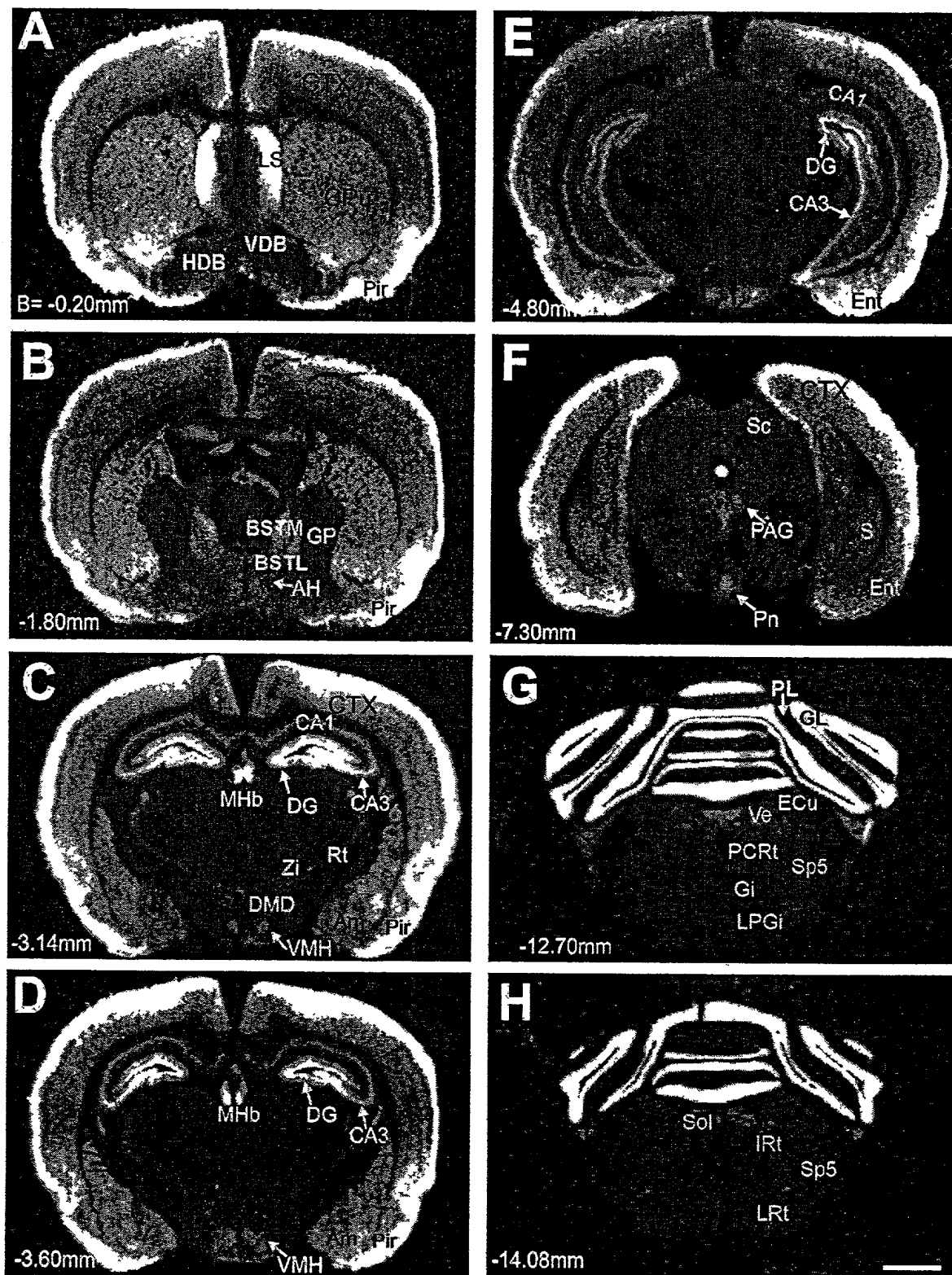


FIGURE 4

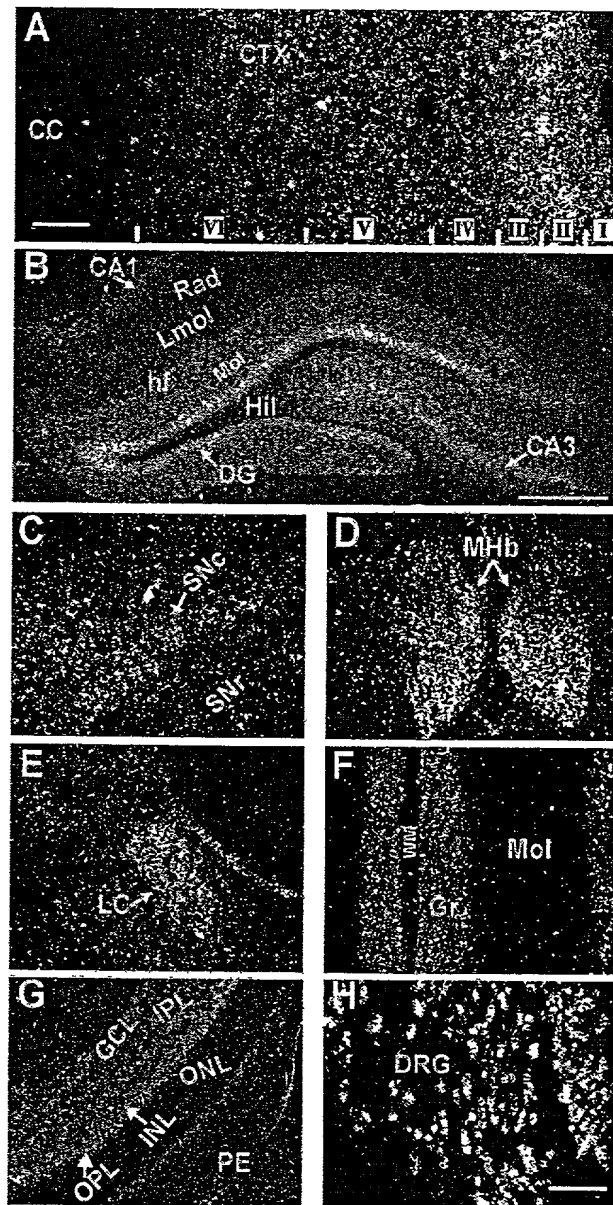


FIGURE 5

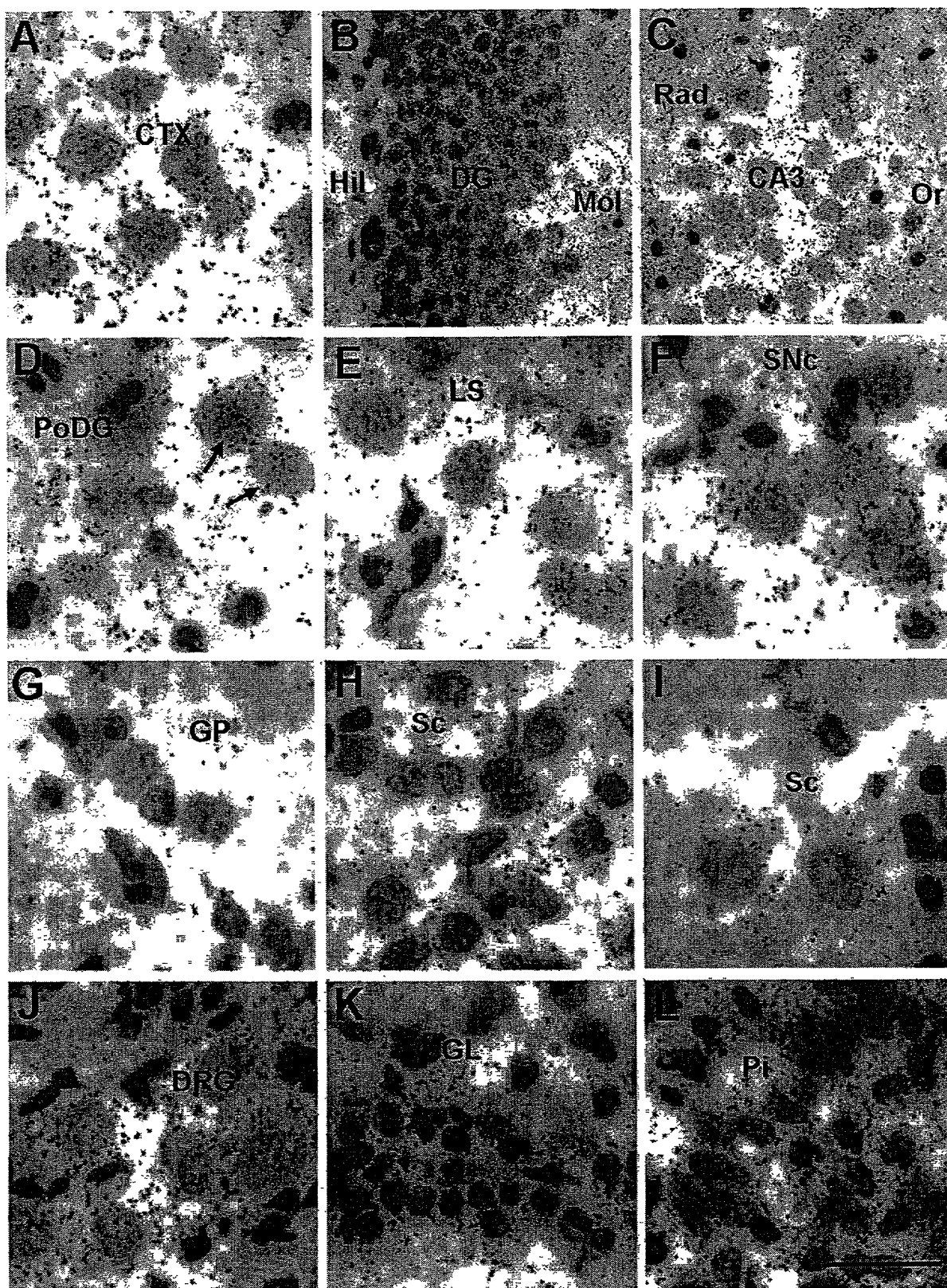


FIGURE 6



1032290 2808080

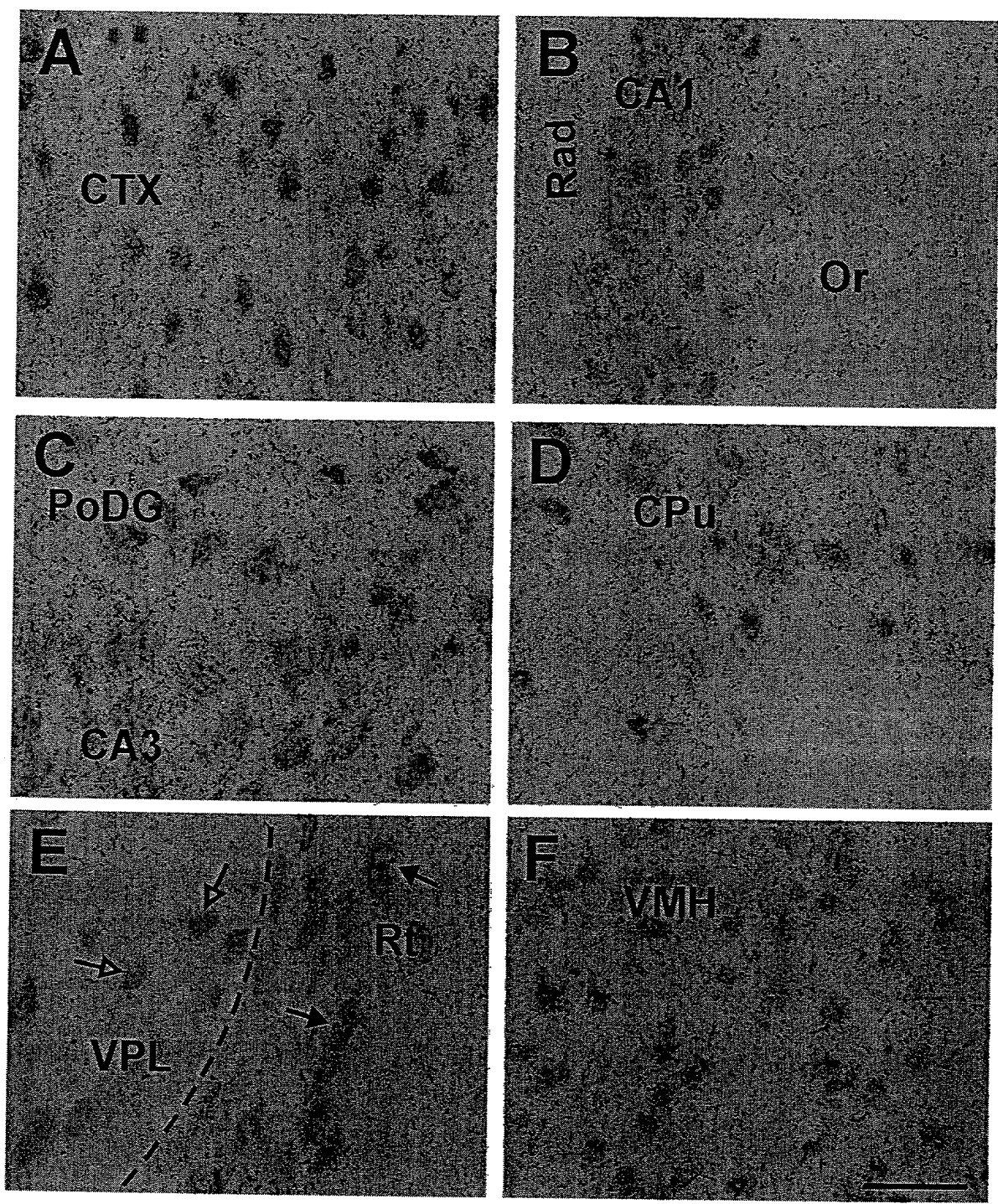


FIGURE 7

05803387.062201

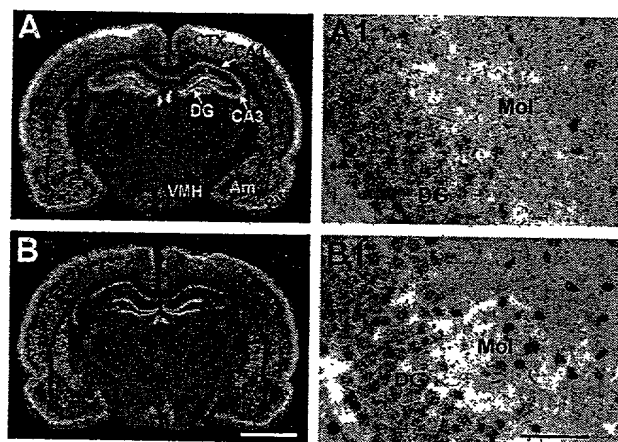


FIGURE 8



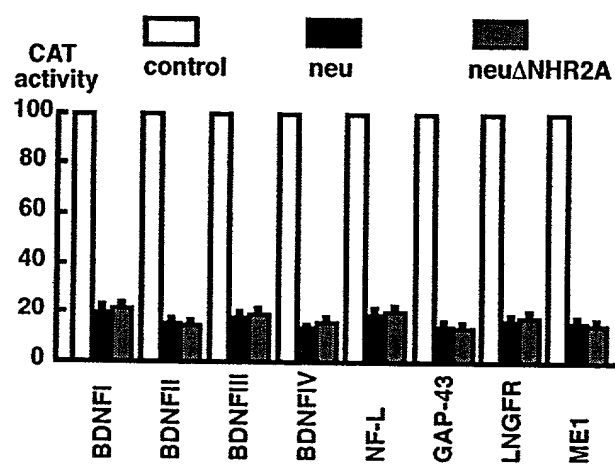


FIGURE 9

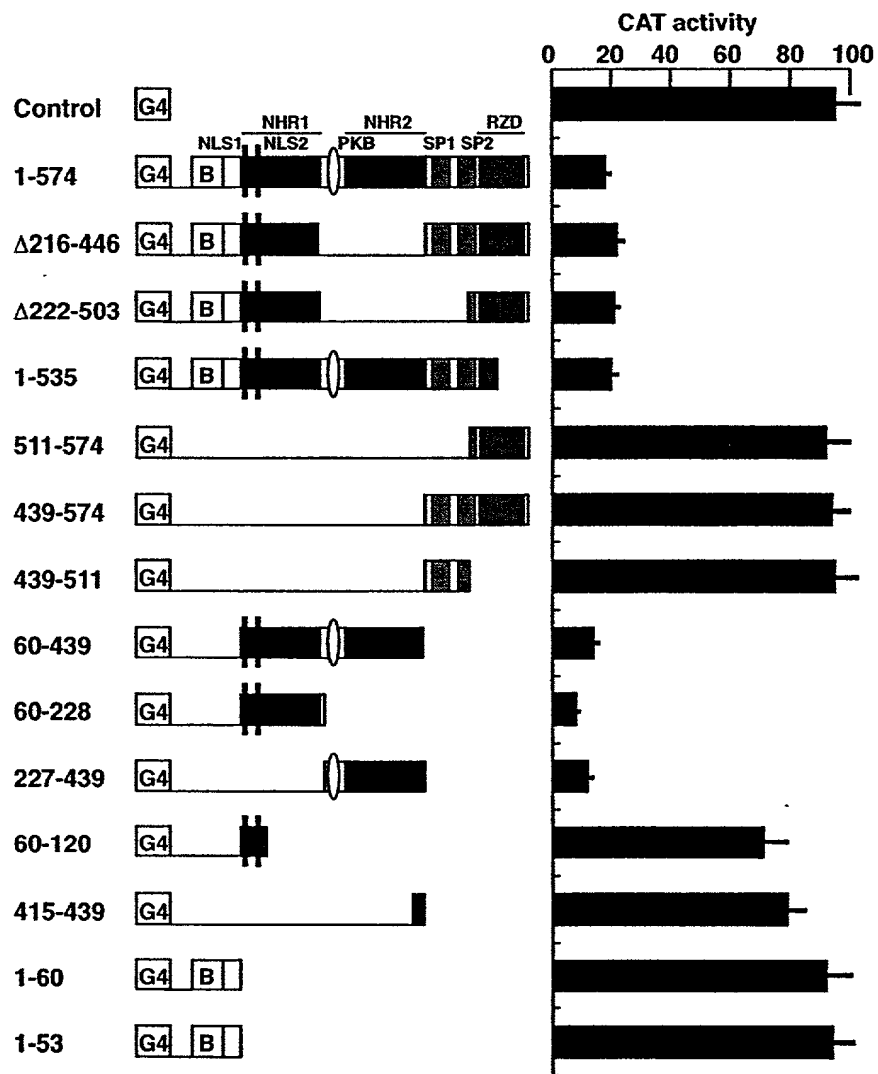


FIGURE 10

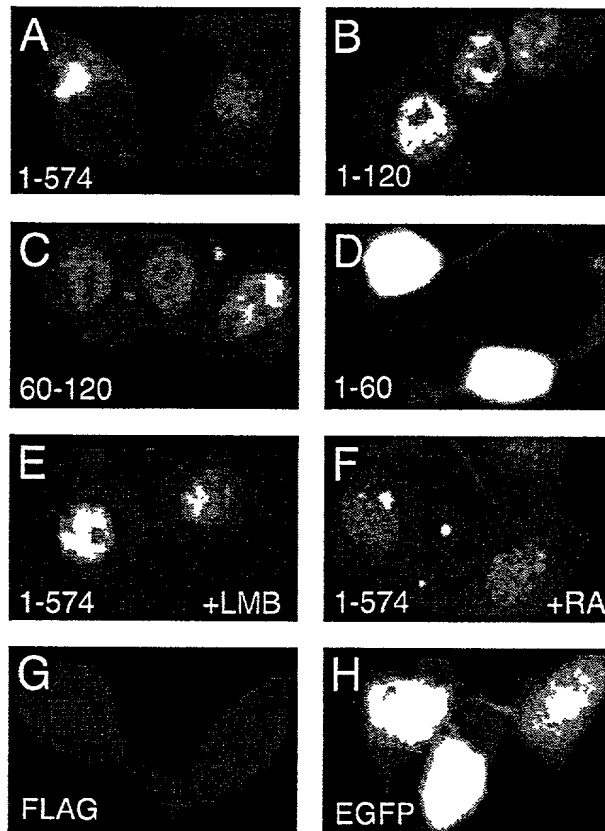


FIGURE 11

h1I FHPHTKGSILMDLSHKAVKR-QASFCNAIFSNRPVLIYEQRKTKKQCCWSCRR  
h2I FHAQAKGKVRIDGHSRRATR-RNSFCNGVFICRPLRYEQRVAVVRPGWSCRR  
h3 FHAQAKGKVRIDTRGCTAHR-RTTFHDGIFICRPLRGERALVLRRESGWCGRR  
dI FHS-VHGDNRSRDGTIARR-FESFCRAIFARDRINERCAEISNNWNGRR  
dII FHNTK-GRNVRISQDRFVSRTESDFCQGYFARPRIKELIAVLKTEQMYVGAA  
h2II FHATR-GPDVSIADRKVACAPRPDGGRTIFERP RPGESLEFGRPGLAAPGAA  
h1II FHALRAGAVRILDEQTVARVEHGRDERALFESRPVVAETEFKTRSGGARPGAA

h1I GTSKPSRHPDSLPHYACPDLVSGFVKAL-PEEFANEENIAFWVDKKCFHRI  
h2I GTAHPSLSAQDIPKYACPDLVTPGYVKAL-PENLALRDTVAIWADRHRGFYSV  
h3 GTRLPAOSVPSLPFFLCPDLEE SPTWAVL-PEGCALTSDLVRFWVDRRGCFKAV  
dI GTSNPEVTLEG-TLPKYACPDLTNPGFVKAL-HEQYCEKONIDYVVNGAGDIYGI  
dII GTSCPAMLPQ-NDLPNDSDFLLDRPEYVVSVDIAAAPQRGDEIAFFVAPNGEISIK  
h2II GTSCPGVLRP-NELPADPDALLKEYVVAR-AGVPVSGGDALSFTLRPGDVLGI  
h1II GVTCPGTLRP-ADLPFSPEALVDRKEFVCR-VPGPLHSGDILGLVVNADGEHLSH

h1I NDSAVMLFFSGVRTADPLWAFVDVYG-LTRGVOLH  
h2I NDGEPVLFHCGVAVGGPLWAFVDVYG-ITDEVOLH  
h3 NAGCRLLLREGVPVGAPLWAFVDVYG-TTKATELL  
dI NNEEKGVILTGDTRSLLTVDVYG-NCTGEEEL  
dII NNGPAVVVMHVDQSLQLWAFVDVYG-STQSERME  
h2II NGRPRGRLLCDDTTQALWAFVARGGVAGQRLD  
h1II NGAAAGMQLCVDASQPLWAFVARGGVAGQRLD

FIGURE 12

	MOUSE										RAT																								
	BRAIN					BRAIN																			HEART	KIDNEY	MUS	SP.LC	THYMUS	TESTIS	LIVER	LUNG	tRNA		
	E13	E15	P0	P8	ad	tRNA	E13	E16	E21	P7	P21	P35	ad	HC	CTX	OLF	STR	THA	HTH	COL	MID	CBL	PONS	MED	SP.C	PIT									
R-NEU2																																			
M-NEU2																																			

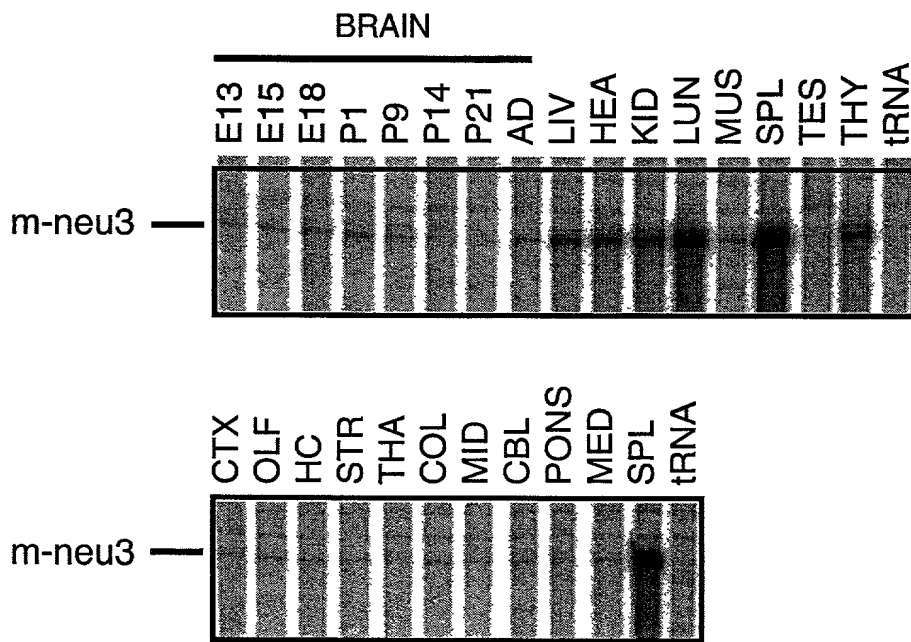


FIGURE 14

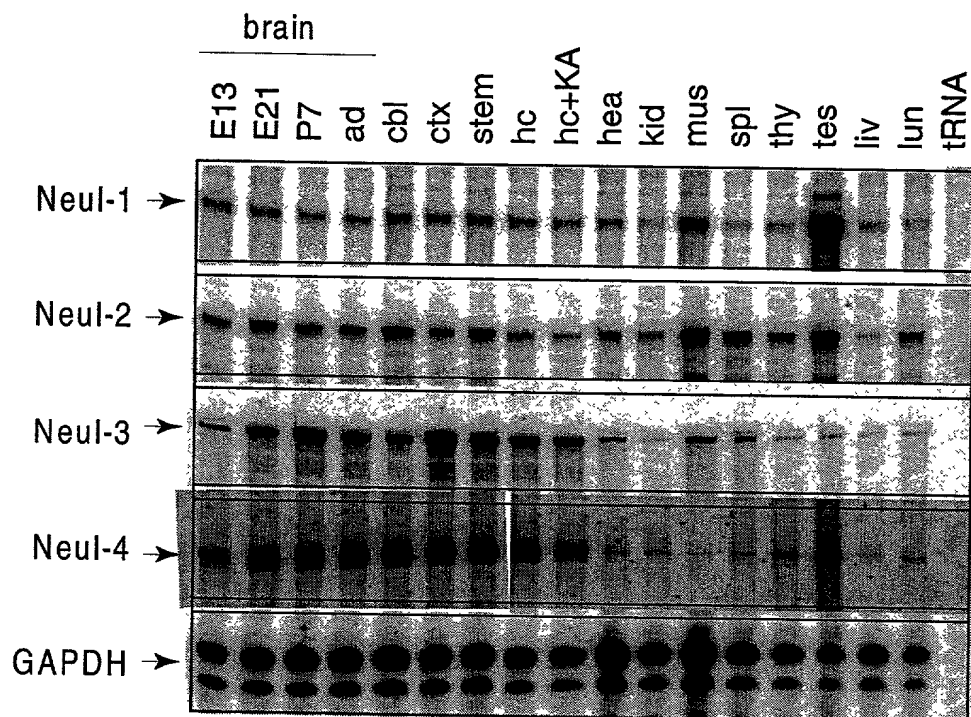


FIGURE 15